

RESEARCH ASSISTANT POSITION IN GENE EXPRESSION ANALYSIS (1 year minimum, up to 3 years)

A 3 year research assistant/associate position focusing on gene expression data analysis is available in the National University of Singapore, to be hosted at the Department of Epidemiology and Public Health in the Yong Loo Lin School of Medicine.

Large scale genetic association studies that adopt an agnostic approach in surveying across the entire human genomic landscape have yielded remarkable successes at identifying common genetic variants that are implicated with variations in blood lipid levels, metabolic traits and other complex human traits. The availability of technologies for genome-wide expression profiling provides the potential for integrating the survey of human variation with both genomic and transcriptional variation. Two aspects of human variations are of particular interest: (i) blood lipid levels – given these are often vital biomarkers for a number of common lifestyle diseases including obesity, diabetes and cardiovascular diseases; (ii) metabolomes – given that these provide clues to cellular physiology and metabolic profiling. The demography of Singapore offers a unique opportunity to survey across these different human landscapes, and to establish a database of normal variation across each of the three population groups in blood lipid and metabolite levels, and to jointly explain these variations with genomic and gene expression variations. Strategically, the Chinese, Malays and Asian Indian groups in Singapore possess the potential to broadly represent almost a third of the global populace, underlining the vast potential and merit this integrated survey of the different omic technologies presents to the scientific community.

The Singapore Natural Variation Project aims to establish baseline characteristics of the normal healthy subjects from each of the three major ethnic groups in Singapore, in the aspects of genomics, transcriptomics, lipidomics/metabolomics and potentially meta-genomics. The focus of the research will be to integrate the data across these different omic technologies to identify patterns of associations to explain variation in expression, lipid or metabolite levels.

The successful applicant is expected to possess a degree in genetics, statistics, computational biology or bioinformatics, and be familiar with file management and data analysis in the Unix/Linux environment. Candidates proficient in PERL programming will be preferred although training will be provided.

The successful applicant will be working directly with YY Teo (statyy@nus.edu.sg), and interested applicants are welcomed to contact YY for more information. A formal application can be made by submitting a resume, cover letter and the names of two potential referees to Inky Lim (ephlimy@nus.edu.sg). The deadline for the application is 15th July 2011.

POSTDOCTORAL POSITION IN GENE EXPRESSION ANALYSIS (1 year minimum, up to 3 years)

A 3 year postdoctoral position focusing on gene expression data analysis is available in the National University of Singapore, to be hosted at the Department of Epidemiology and Public Health in the Yong Loo Lin School of Medicine.

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The successful applicant is expected to possess a PhD in genetics, statistics, computational biology or bioinformatics, and with considerable programming experience within the Unix/Linux environment in PERL and either Java or C/C++.

The successful applicant will be working directly with YY Teo (statyy@nus.edu.sg), and interested applicants are welcomed to contact YY for more information. A formal application can be made by submitting a resume, cover letter and the names of two potential referees to Inky Lim (ephlimy@nus.edu.sg). The deadline for the application is 15th July 2011.